SEQUENCE LISTING

_	(1) GENERAL INFORMATION:
5	(i) APPLICANT: Madison, Edwin L
10	(ii) TITLE OF INVENTION: TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA VARIANTS HAVING ZYMOGEN CHARACTERISTICS: COMPOSITIONS AND METHODS OF USE
	(iii) NUMBER OF SEQUENCES: 1
15	 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff (B) STREET: 300 South Wacker Drive, 32nd Floor (C) CITY: Chicago (D) STATE: IL
20	(E) COUNTRY: USA (F) ZIP: 60606
25	 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
30	<pre>(vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:</pre>
35	<pre>(viii) ATTORNEY/AGENT INFORMATION:</pre>
40	(ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 312-913-0001 (B) TELEFAX: 312-913-0002
	(2) INFORMATION FOR SEQ ID NO:1:
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant
50	(ii) MOLECULE TYPE: peptide
	(iii) HYPOTHETICAL: NO
55	(iv) ANTI-SENSE: NO
	(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

	(xi)	SE	UENC	E DES	CRIE	PTION	l: SE	EQ II	NO:	1:						
5	Sei 1	Ту	Gln	Val	Ile 5	Cys	Arg	Asp	Glu	Lys 10	Thr	Gln	Met	Ile	Tyr 15	Gln
10	Glı	n His	Gln	Ser 20	Trp	Leu	Arg	Pro	Val 25	Leu	Arg	Ser	Asn	Arg 30	Val	Glu
10	Ty	Cy:	Trp 35	Cys	Asn	Ser	Gly	Arg 40	Ala	Gln	Cys	His	Ser 45	Val	Pro	Val
15	Ly	50	Cys	Ser	Glu	Pro	Arg 55	Cys	Phe	Asn	Gly	Gly 60	Thr	Cys	Gln	Gln
	Ala 65	ı Lei	ı Tyr	Phe	Ser	Asp 70	Phe	Val	Cys	Gln	Cys 75	Pro	Glu	Gly	Phe	Ala 80
20	Gl	/ Ly:	cys	Cys	Glu 85	Ile	Asp	Thr	Arg	Ala 90	Thr	Cys	Tyr	Glu	Asp 95	Gln
25	Gl	/ Il	e Ser	Tyr 100	Arg	Gly	Thr	Trp	Ser 105	Thr	Ala	Glu	Ser	Gly 110	Ala	Glu
25	Су	s Th	Asn 115	Trp	Asn	Ser	Ser	Ala 120	Leu	Ala	Gln	Lys	Pro 125	Tyr	Ser	Gly
30	Ar	g Ar	g Pro	Asp	Ala	Ile	Arg 135	Leu	Gly	Leu	Gly	Asn 140	His	Asn	Tyr	Сув
	Ar 14		n Pro	Asp	Arg	Asp 150	Ser	Lys	Pro	Trp	Cys 155	Tyr	Val	Phe	Lys	Ala 160
35	Gl	у Lу	s Tyr	Ser	Ser 165	Glu	Phe	Cys	Ser	Thr 170	Pro	Ala	Cys	Ser	Glu 175	Gly
40	As	n Se	r Asp	Cys 180	Tyr	Phe	Gly	Asn	Gly 185	Ser	Ala	Tyr	Arg	Gly 190	Thr	His
40	Se	r Le	u Thr 195		Ser	Gly	Ala	Ser 200	Cys	Leu	Pro	Trp	Asn 205	Ser	Met	Ile
45	Le	u Il 21	e Gly 0	Lys	Val	Tyr	Thr 215		Gln	Asn	Pro	Ser 220	Ala	Gln	Ala	Leu
	G1 22	_	u Gly	. Tàs	His	Asn 230		Сув	Arg	Asn	Pro 235	Asp	Gly	qaA	Ala	Lys 240
50	Pı	o Tr	p Cys	His	Val 245		Lys	Asn	Arg	Arg 250	Leu	Thr	Trp	Glu	Tyr 255	Cys
55	As	p Va	l Pro	Ser 260	_	Ser	Thr	Сув	Gly 265		Arg	Gln	Tyr	Ser 270		Pro
رر	G;	.n .Pl	ne Glu 275		Lys	Gly	Gly	280		. Ala	Asp	Ile	Ala 285		His	Pro
	T	p G	in Ala	a Ala	ı Ile	Phe	. Ala	Lys	His	arg	Arg	Ser	Pro	Gly	Glu	Arg

		290					295					300				
5	Phe 305	Leu	Cys	Gly	Gly	Ile 310	Leu	Ile	Ser	Ser	Cys 315	Trp	Ile	Leu	Ser	Ala 320
J	Ala	His	Cys	Phe	Gln 325	Glu	Arg	Phe	Pro	Pro 330	His	His	Leu	Thr	Val 335	Ile
10	Leu	Gly	Arg	Thr 340	Tyr	Arg	Val	Val	Pro 345	Gly	Glu	Glu	Glu	Gln 350	Lys	Phe
	Glu	Val	Glu 355	Lys	Tyr	Ile	Val	His 360	Lys	Glu	Phe	Asp	Asp 365	Asp	Thr	Tyr
15	Asp	Asn 370	Asp	Ile	Ala	Leu	Leu 375	Gln	Leu	Lys	Ser	Asp 380	Ser	Ser	Arg	Cys
20	Ala 385	Gln	Glu	Ser	Ser	Val 390	Val	Arg	Thr	Val	Cys 395	Leu	Pro	Pro	Ala	Asp 400
	Leu	Gln	Leu	Pro	Asp 405	Trp	Thr	Glu	Cys	Glu 410	Leu	Ser	Gly	Tyr	Gly 415	Lys
25	Asp	Glu	Ala	Leu 420	Ser	Pro	Phe	Tyr	Ser 425	Glu	Arg	Leu	Lys	Glu 430	Ala	His
	Val	Arg	Leu 435	Tyr	Pro	Ser	Ser	Arg 440	Cys	Thr	Ser	Gln	His 445	Leu	Leu	Asn
30	Arg	Thr 450	Val	Thr	Asp	Asn	Met 455	Leu	Cys	Ala	Gly	Asp 460	Thr	Arg	Ser	Gly
35	Gly 465	Pro	Gln	Ala	Asn	Leu 470	His	Asp	Ala	Cys	Gln 475	Gly	Asp	Ser	Gly	Gly 480
	Pro	Leu	Val	Cys	Leu 485	Asn	Asp	Gly	Arg	Met 490	Thr	Leu	Val	Gly	Ile 495	Ile
40	Ser	Trp	Gly	Leu 500	Gly	Cys	Gly	Gln	Lys 505	Asp	Val	Pro	Gly	Val 510	Tyr	Thr
	Lys	Val	Thr 515	Asn	Tyr	Leu	Asp	Trp 520	Ile	Arg	Asp	Asn	Met 525	Arg	Pro	
45	2) INFOR	OITAN	ON FO	OR SI	EQ II	ОИО	:2:									
50	(i)	(B)	LEI TYI	NGTH PE: { RAND!	ARACT 52' amino EDNES 3Y: 1	7 am: 5 ac: 55: 1	ino a id not :	acid: relev								
	(ii)	MOLI	ECULI	E TY	PE:]	pept:	ide									
55	(iii)	НУР	OTHE'	TICA	L: N	0										
	(iv)	ANT	I-SE	NSE:	NO											

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5	(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	2:						
	Ser 1	Tyr	Gln '		Ile 5	Cys	Arg	Asp	Glu	Lys 10	Thr	Gln	Met	Ile	Tyr 15	Gln
10	Gln	His		Ser 20	Trp	Leu	Arg	Pro	Val 25	Leu	Arg	Ser	Asn	Arg 30	Val	Glu
	Tyr	Cys	Trp 35	Cys	Asn	Ser	Gly	Arg 40	Ala	Gln	Cys	His	Ser 45	Val	Pro	Val
15	Lys	Ser 50	Сув	Ser	Glu	Pro	Arg 55	Cys	Phe	Asn	Gly	Gly 60	Thr	Cys	Gln	Gln
20	Ala 65	Leu	Tyr	Phe	Ser	Asp 70	Phe	Val	Cys	Gln	Cys 75	Pro	Glu	Gly	Phe	Ala 80
	Gly	Lys	Cys	Cys	Glu 85	Ile	Asp	Thr	Arg	Ala 90	Thr	Cys	Tyr	Glu	Asp 95	Gln
25	Gly	Ile	Ser	Tyr 100	Arg	Gly	Thr	Trp	Ser 105	Thr	Ala	Glu	Ser	Gly 110	Ala	Glu
	Cys	Thr	Asn 115	Trp	Asn	Ser	Ser	Ala 120	Leu	Ala	Gln	Lys	Pro 125	Tyr	Ser	Gly
30	Arg	Arg 130	Pro	Asp	Ala	Ile	Arg 135	Leu	Gly	Leu	Gly	Asn 140	His	Asn	Tyr	Cys
35	Arg 145	Asn	Pro	Asp	Arg	Asp 150	Ser	Lys	Pro	Trp	Cys 155	Tyr	Val	Phe	Lys	Ala 160
	Gly	Lys	Tyr	Ser	Ser 165	Glu	Phe	Cys	Ser	Thr 170	Pro	Ala	Суз	Ser	Glu 175	Gly
40	Asn	Ser	Asp	Cys 180	Tyr	Phe	Gly	Asn	Gly 185		Ala	Tyr	Arg	Gly 190	Thr	His
	Ser	Leu	Thr 195	Glu	Ser	Gly	Ala	Ser 200		Leu	Pro	Trp	Asn 205	Ser	Met	Ile
45	Lev	1 lle 210	-	Lys	Val	Тут	Thr 215		Glr	Asn	Pro	Ser 220		Gln	Ala	Leu
50	Gl ₃ 229	/ Leu	Gly	Lys	His	230		Cys	arç	g Asn	235		Gly	Asp	Ala	Lys 240
	Pro	o Trp	Cys	His	Va]		ı Ly:	s Ası	n Arg	g Arg 250		Thr	Trp	Glu	255	Cys
55	As	p Val	Pro	Ser 260		s Se:	r Th	r Cyi	3 Gl		ı Arç	g Glr	туз	5ei 270		n Pro
	Gl	n Phe	e Glu 279		e Ly:	s Gl	y Gl	y Le ²		e Ala	a Asp) Ile	285	a Se	r His	s Pro

	Trp	Gln 290	Ala	Ala	Ile	Phe	Ala 295	Lys	His	Arg	Arg	Ser 300	Pro	Gly	Glu	Arg
5	Phe 305	Leu	Cys	Gly	Gly	Ile 310	Leu	Ile	Ser	Ser	Cys 315	Trp	Ile	Leu	Ser	Ala 320
10	Ala	His	Cys	Phe	Gln 325	Glu	Arg	Phe	Pro	Pro 330	His	His	Leu	Thr	Val 335	Ile
10	Leu	Gly	Arg	Thr 340	Tyr	Arg	Val	Val	Pro 345	Gly	Glu	Glu	Glu	Gln 350	Lys	Phe
15	Glu	Val	Glu 355	Lys	Tyr	Ile	Val	His 360	Lys	Glu	Phe	Asp	Asp 365	Asp	Thr	Tyr
	Asp	Asn 370	Asp	Ile	Ala	Leu	Leu 375	Gln	Leu	Lys	Ser	Asp 380	Ser	Ser	Arg	Cys
20	Ala 385	Gln	Glu	Ser	Ser	Val 390	Val	Arg	Thr	Val	Cys 395	Leu	Pro	Pro	Ala	Asp 400
25	Leu	Gln	Leu	Pro	Asp 405	Trp	Thr	Glu	Cys	Glu 410	Leu	Ser	Gly	Tyr	Gly 415	Lys
23	Glu	Glu	Ala	Leu 420	Ser	Pro	Phe	Tyr	Ser 425	Glu	Arg	Leu	Lys	Glu 430	Ala	His
30	Val	Arg	Leu 435	Tyr	Pro	Ser	Ser	Arg 440	Сув	Thr	Ser	Gln	His 445	Leu	Leu	Asn
	Arg	Thr 450	Val	Thr	Asp	Asn	Met 455	Leu	Cys	Ala	Gly	Asp 460	Thr	Arg	Ser	Gly
35	Gly 465	Pro	Gln	Ala	Asn	Leu 470	His	Asp	Ala	Cys	Gln 475	Gly	Asp	Ser	Gly	Gly 480
40	Pro	Leu	Val	Cys	Leu 485	Asn	Asp	Gly	Arg	Met 490	Thr	Leu	Val	Gly	Ile 495	Ile
40	Ser	Trp	Gly	Leu 500	Gly	Cys	Gly	Gln	Lys 505	Asp	Val	Pro	Gly	Val 510	Tyr	Thr
45	Lys	val	Thr 515		Tyr	Leu	Asp	Trp 520		Arg	Asp	Asn	Met 525	Arg	Pro	
	2) INFOR	ITAMS	ON F	OR S	EQ I	D NO	:3:									
50	(i)		L) LE	E CH NGTH	: 52	7 aπ	ino		ls							
55		(0	c) si	RAND POLC	EDNE	:SS:	not			:						
55	(ii)) - MOI	ECUI	LE TY	PE:	pept	ide									

(iii) HYPOTHETICAL: NO

•	(iv) ANTI-SENSE: NO	
	(vi) ORIGINAL SOURCE:	
5	(A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
10	Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln 1 10 15	L
1.6	Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu 20 25 30	L
15	Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val 35 40 45	-
20	Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln 50 55 60	1
	Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala 70 75 80	ì
25	Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln 85 90 95	1
	Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu 100 105 110	1
30	Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly	7
35	Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys 130 135 140	3
	Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala 145 150 155 160	
40	Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly 165 170 175	Y
	Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His	S
45	Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile 195 200 205	е
50	Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Le 210 215 220	u
	Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Ly 225 230 235 24	
55	Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cy 245 250 255	's

Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro

265

270

260

55

	Gln	Phe	Glu 275	Ile	Lys	Gly	Gly	Leu 280	Phe	Ala	Asp	Ile	Ala 285	Ser	His	Pro
5	Trp	Gln 290	Ala	Ala	Ile	Phe	Ala 295	Lys	His	Arg	Arg	Ser 300	Pro	Gly	Glu	Arg
10	Phe 305	Leu	Cys	Gly	Gly	Ile 310	Leu	Ile	Ser	Ser	Cys 315	Trp	Ile	Leu	Ser	Ala 320
10	Ala	His	Cys	Phe	Gln 325	Glu	Arg	Phe	Pro	Pro 330	His	His	Leu	Thr	Val 335	Ile
15	Leu	Gly	Arg	Thr 340	Tyr	Arg	Val	Val	Pro 345	Gly	Glu	Glu	Glu	Gln 350	Lys	Phe
	Glu	Val	Glu 355	Lys	Tyr	Ile	Val	His 360	Lys	Glu	Phe	Asp	Asp 365	Asp	Thr	Tyr
20	Asp	Asn 370	Asp	Ile	Ala	Leu	Leu 375	Gln	Leu	Lys	Ser	Asp 380	Ser	Ser	Arg	Cys
25	Ala 385	Gln	Glu	Ser	Ser	Val 390	Val	Arg	Thr	Val	Cys 395	Leu	Pro	Pro	Ala	Asp 400
23	Leu	Gln	Leu	Pro	Asp 405	Trp	Thr	Glu	Cys	Glu 410	Leu	Ser	Gly	Tyr	Gly 415	Lys
30	His	Glu	Ala	Leu 420	Ser	Pro	Phe	Tyr	Ser 425	Glu	Arg	Leu	Tyr	Glu 430	Ala	His
	Val	Arg	Leu 435		Pro	Ser	Ser	Arg 440	Cys	Thr	Ser	Gln	His 445	Leu	Leu	Asn
35	Arg	Thr 450		Thr	Asp	Asn	Met 455		Cys	Ala	Gly	Asp 460	Thr	Arg	Ser	Gly
40	Gly 465	Pro	Gln	Ala	Asn	Leu 470		Asp	Ala	Cys	Gln 475	Gly	Asp	Ser	Gly	Gly 480
40	Pro	Leu	Val	Cys	Leu 485		Asp	Gly	Arg	Met 490	Thr	Leu	Val	Gly	Ile 495	Ile
45	Sei	Trp	Gly	Leu 500		Cys	Gly	Gln	Lys 505		Val	Pro	Gly	Val 510		Thr
	Lys	s Val	Thr 515		Туг	Leu	Asp	Trp 520		Arg	Asp	Asn	Met 525		Pro	
50	2) INF	ORMAT	rion	FOR	SEQ	ID N	iO : 4 :									
	(i) SE(_	CE CH												

(B) TYPE: nucleic acid

(ii) MOLECULE TYPE: cDNA

(C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant

	(iii) HYPOTHETICAL: NO	
5	(iv) ANTI-SENSE: NO	
3	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	CTACGGCAAG CATGAGGCCT TGTCTCCTTT CTATTCGGAG CGGCTGAAGG AGGCTCATGT	60
15	CAGACTGTAC CCATCCAGCC GCTGCACATC ACAACATTTA CTTAACAGAA CAGTCACCGA	120
	CAACATGCTG TGTGCTGGAG ACACTCGGAG CGGCGGGCCC CAGGCAAACT TGCACGACGC	180
20	CTGCCAGGGC GATTCGGGAG GCCCCCTGGT GTGTCTGAAC GATGGCCGCA TGACTTTGGT	240
20	GGGCATCATC AGCTGGGGCC TGGGCTGTGG ACAGAAGGAT GTCCCGGGTG	290
25	(2) INFORMATION FOR SEQ ID NO:5:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 290 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
	(ii) MOLECULE TYPE: cDNA	
	(iii) HYPOTHETICAL: NO	
35	(iv) ANTI-SENSE: NO	
	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
40	(M) ORGANIZET. Homo Dupicus	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
45	CTACGGCAAG GACGAGGCCT TGTCTCCTTT CTATTCGGAG CGGCTGAAGG AGGCTCATGT	60
	CAGACTGTAC CCATCCAGCC GCTGCACATC ACAACATTTA CTTAACAGAA CAGTCACCGA	120
50	CAACATGCTG TGTGCTGGAG ACACTCGGAG CGGCGGGCCC CAGGCAAACT TGCACGACGC	180
50	CTGCCAGGGC GATTCGGGAG GCCCCCTGGT GTGTCTGAAC GATGGCCGCA TGACTTTGGT	240
	GGGCATCATC AGCTGGGGCC TGGGCTGTGG ACAGAAGGAT GTCCCGGGTG	290
55	(2) INFORMATION FOR SEQ ID NO:6:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs

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290

	(B) TYPE: nucleic acid(C) STRANDEDNESS: not relevant(D) TOPOLOGY: not relevant	
5	(ii) MOLECULE TYPE: cDNA	
	(iii) HYPOTHETICAL: NO	
10	(iv) ANTI-SENSE: NO	
10	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
	CTACGGCAAG GAGGAGGCCT TGTCTCCTTT CTATTCGGAG CGGCTGAAGG AGGCTCATGT	60
20	CAGACTGTAC CCATCCAGCC GCTGCACATC ACAACATTTA CTTAACAGAA CAGTCACCGA	120
	CAACATGCTG TGTGCTGGAG ACACTCGGAG CGGCGGGCCC CAGGCAAACT TGCACGACGC	180
25	CTGCCAGGGC GATTCGGGAG GCCCCCTGGT GTGTCTGAAC GATGGCCGCA TGACTTTGGT	240
23	GGGCATCATC AGCTGGGGCC TGGGCTGTGG ACAGAAGGAT GTCCCGGGTG	290
30	(2) INFORMATION FOR SEQ ID NO:7:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 290 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
	(ii) MOLECULE TYPE: cDNA	
	(iii) HYPOTHETICAL: NO	
40	(iv) ANTI-SENSE: NO	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
50	CTACGGCAAG CATGAGGCCT TGTCTCCTTT CTATTCGGAG CGGCTGTATG AGGCTCATGT	60
	CAGACTGTAC CCATCCAGCC GCTGCACATC ACAACATTTA CTTAACAGAA CAGTCACCGA	120
55	CAACATGCTG TGTGCTGGAG ACACTCGGAG CGGCGGGCCC CAGGCAAACT TGCACGACGC	180
55	CTGCCAGGGC GATTCGGGAG GCCCCCTGGT GTGTCTGAAC GATGGCCGCA TGACTTTGGT	240

GGGCATCATC AGCTGGGGCC TGGGCTGTGG ACAGAAGGAT GTCCCGGGTG

	(2) INFORMATION FOR SEQ ID NO:8:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
10	(ii) MOLECULE TYPE: cDNA	
	(iii) HYPOTHETICAL: NO	
15	(iv) ANTI-SENSE: NO	
15	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
	CTACGGCAAG GACGAGGCCT TGT	23
25	(2) INFORMATION FOR SEQ ID NO:9:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
25	(ii) MOLECULE TYPE: cDNA	
35	(iii) HYPOTHETICAL: NO	
	(iv) ANTI-SENSE: NO	
40	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
	CTACGGCAAG GAGGAGGCCT TGT	23
50	(2) INFORMATION FOR SEQ ID NO:10:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	

(ii) MOLECULE TYPE: cDNA

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- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- 5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGAGCGGCT GTATGAGGCT MCATGT

25